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Poster Abstract - C.63

NUCLEOTIDE DIVERSITY, LINKAGE DISEQUILIBRIUM AND POPULATION DIFFERENTIATION IN A SET OF CANDIDATE GENES FOR TIME OF BUD SET IN NORWAY SPRUCE (*PICEA ABIES)*

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Conifers appear to have sufficient nucleotide diversity and rapid decay of linkage disequilibrium to make allele-phenotype association mapping studies based on candidate genes an attractive approach for the dissection of complex traits. Furthermore the low levels of between population differentiation that were previously observed for neutral markers are expected to significantly alleviate the problem of false positive associations due to population substructuring, one of the major drawbacks in association mapping. In order to evaluate this mapping method based on variation in natural populations we set out to perform an association mapping study in Norway Spruce (*Picea abies*) intended to unveil the genetic factors controlling bud set time and length of seasonal growth. These traits show high heritability in spruce and strong differentiation along latitudinal clines. Candidate genes were chosen among those involved in the light-dependent control of the length of the vegetative season in *Arabidopsis* and other model species. Candidate genes and a set of reference loci were resequenced in seven European populations of Norway spruce distributed over the latitudinal cline observed for bud set. Here we present and discuss the results on the distribution of single nucleotide polymorphisms (SNPs) and the levels of short range linkage disequilibrium observed in the selected loci. Moreover a preliminary analysis of among-populations genetic differentiation will be presented with regard to its potential effects on the association study. The comparison of nucleotide diversity data with phenotypic data may be used to detect significant associations between molecular markers and phenotype and determine the role of the loci analyzed.